



SEQUENCE LISTING

<110> Ware, Carl F.

<120> LIGAND FOR HERPES SIMPLEX VIRUS ENTRY MEDIATOR AND METHODS OF USE

<130> 051501/0276397

<140> 09/549,096

<141> April 12, 2000

<160> 6

<170> PatentIn Ver. 2.0

<210> 1

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Forward primer sequence

<400> 1

cggagatctg agttcatcct gctagctgg

29

<210> 2

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Backward primer sequence

<400> 2

ataggatccc ttggtctggt gctgacattc c

31

<210> 3

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Forward primer sequence

<400> 3

gacgtcagat cttccacct ttctctcta

29

<210> 4

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Backward primer sequence

RECEIVED

JUN 26 2001

TECH CENTER 1600/2900

<400> 4
gaacagagat ctcattgctc ctggctctg

29

<210> 5
<211> 1169
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (49)..(771)

<400> 5
gaggttgaag gacccaggcg tgtcagccct gctccagaga ccttgggc atg gag gag 57
Met Glu Glu

1
agt gtc gta cgg ccc tca gtg ttt gtg gtg gat gga cag acc gac atc 105
Ser Val Val Arg Pro Ser Val Phe Val Val Asp Gly Gln Thr Asp Ile

5 10 15
cca ttc acg agg ctg gga cga agc cac cgg aga cag tcg tgc agt gtg 153
Pro Phe Thr Arg Leu Gly Arg Ser His Arg Arg Gln Ser Cys Ser Val

20 25 30 35
gcc cgg gtg ggt ctg ggt ctc ttg ctg ttg ctg atg ggg gct ggg ctg 201
Ala Arg Val Gly Leu Gly Leu Leu Leu Leu Leu Met Gly Ala Gly Leu

40 45 50
gcc gtc caa ggc tgg ttc ctc ctg cag ctg cac tgg cgt cta gga gag 249
Ala Val Gln Gly Trp Phe Leu Leu Gln Leu His Trp Arg Leu Gly Glu

55 60 65
atg gtc acc cgc ctg cct gac gga cct gca ggc tcc tgg gag cag ctg 297
Met Val Thr Arg Leu Pro Asp Gly Pro Ala Gly Ser Trp Glu Gln Leu

70 75 80
ata caa gag cga agg tct cac gag gtc aac cca gca gcg cat ctc aca 345
Ile Gln Glu Arg Arg Ser His Glu Val Asn Pro Ala Ala His Leu Thr

85 90 95
ggg gcc aac tcc agc ttg acc ggc agc ggg ggg ccg ctg tta tgg gag 393
Gly Ala Asn Ser Ser Leu Thr Gly Ser Gly Gly Pro Leu Leu Trp Glu

100 105 110 115
act cag ctg ggc ctg gcc ttc ctg agg ggc ctc agc tac cac gat ggg 441
Thr Gln Leu Gly Leu Ala Phe Leu Arg Gly Leu Ser Tyr His Asp Gly

120 125 130
gcc ctt gtg gtc acc aaa gct ggc tac tac tac atc tac tcc aag gtg 489

Ala Leu Val Val Thr Lys Ala Gly Tyr Tyr Tyr Ile Tyr Ser Lys Val
 135 140 145
 cag ctg ggc ggt gtg ggc tgc ccg ctg ggc ctg gcc agc acc atc acc 537
 Gln Leu Gly Gly Val Gly Cys Pro Leu Gly Leu Ala Ser Thr Ile Thr
 150 155 160
 cac ggc ctc tac aag cgc aca ccc cgc tac ccc gag gag ctg gag ctg 585
 His Gly Leu Tyr Lys Arg Thr Pro Arg Tyr Pro Glu Glu Leu Glu Leu
 165 170 175
 ttg gtc agc cag cag tca ccc tgc gga cgg gcc acc agc agc tcc cgg 633
 Leu Val Ser Gln Gln Ser Pro Cys Gly Arg Ala Thr Ser Ser Ser Arg
 180 185 190 195
 gtc tgg tgg gac agc agc ttc ctg ggt ggt gtg gta cac ctg gag gct 681
 Val Trp Trp Asp Ser Ser Phe Leu Gly Gly Val Val His Leu Glu Ala
 200 205 210
 ggg gag gag gtg gtc gtc cgt gtg ctg gat gaa cgc ctg gtt cga ctg 729
 Gly Glu Glu Val Val Val Arg Val Leu Asp Glu Arg Leu Val Arg Leu
 215 220 225
 cgt gat ggt acc cgg tct tac ttc ggg gct ttc atg gtg tga 771
 Arg Asp Gly Thr Arg Ser Tyr Phe Gly Ala Phe Met Val
 230 235 240
 aggaaggagc gtggtgcatt ggacatgggt ctgacacgtg gagaactcag aggggtgcctc 831
 aggggaaaga aaactcacga agcagaggct gggcgtggtg gctctgcct gtaatcccag 891
 cactttggga ggccaaggca ggcggatcac ctgaggtcag gagttcgaga ccagcctggc 951
 taacatggca aaaccccatc tctactaaaa atacaaaaat tagccggacg tgggtggtgcc 1011
 tgcctgtaat ccagctactc aggaggctga ggcaggataa ttttgcttaa acccgggagg 1071
 cggaggttgc agtgagccga gatcacacca ctgcactcca acctgggaaa cgcagtgaga 1131
 ctgtgcctca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1169

<210> 6

<211> 240

<212> PRT

<213> Homo sapiens

<400> 6

Met Glu Glu Ser Val Val Arg Pro Ser Val Phe Val Val Asp Gly Gln
 1 5 10 15
 Thr Asp Ile Pro Phe Thr Arg Leu Gly Arg Ser His Arg Arg Gln Ser
 20 25 30

Cys Ser Val Ala Arg Val Gly Leu Gly Leu Leu Leu Leu Leu Met Gly			
35	40	45	
Ala Gly Leu Ala Val Gln Gly Trp Phe Leu Leu Gln Leu His Trp Arg			
50	55	60	
Leu Gly Glu Met Val Thr Arg Leu Pro Asp Gly Pro Ala Gly Ser Trp			
65	70	75	80
Glu Gln Leu Ile Gln Glu Arg Arg Ser His Glu Val Asn Pro Ala Ala			
85	90	95	
His Leu Thr Gly Ala Asn Ser Ser Leu Thr Gly Ser Gly Gly Pro Leu			
100	105	110	
Leu Trp Glu Thr Gln Leu Gly Leu Ala Phe Leu Arg Gly Leu Ser Tyr			
115	120	125	
His Asp Gly Ala Leu Val Val Thr Lys Ala Gly Tyr Tyr Tyr Ile Tyr			
130	135	140	
Ser Lys Val Gln Leu Gly Gly Val Gly Cys Pro Leu Gly Leu Ala Ser			
145	150	155	160
Thr Ile Thr His Gly Leu Tyr Lys Arg Thr Pro Arg Tyr Pro Glu Glu			
165	170	175	
Leu Glu Leu Leu Val Ser Gln Gln Ser Pro Cys Gly Arg Ala Thr Ser			
180	185	190	
Ser Ser Arg Val Trp Trp Asp Ser Ser Phe Leu Gly Gly Val Val His			
195	200	205	
Leu Glu Ala Gly Glu Glu Val Val Val Arg Val Leu Asp Glu Arg Leu			
210	215	220	
Val Arg Leu Arg Asp Gly Thr Arg Ser Tyr Phe Gly Ala Phe Met Val			
225	230	235	240